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RESULT 5
AAW31706
ID   AAW31706 standard; protein; 1363 AA.
XX
AC   AAW31706;
XX
DT   16-JUN-2003  (revised)
DT   25-MAR-2003  (revised)
DT   14-APR-1999  (first entry)
XX
DE   Bovine coronavirus E2 (S) protein.
XX
KW   BCV; E2 protein; peplomer protein; S spike; antigen; vaccine; cattle;
KW   BOND_P2; S peplomer polypeptide precursor;
KW   S peplomer polypeptide precursor [Bovine coronavirus];
KW   spike glycoprotein; spike glycoprotein [bovine coronavirus]; G05529;
KW   G05944; G09405; G016020; G016021; G019031; G019061; G019064; G046789;
KW   G046813.
XX
OS   Bovine coronavirus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .17
FT                   /label= Sig_peptide
FT   Protein         18. .1363
FT                   /label= Mat_protein
FT   Domain          1306. .1338
FT                   /note= "transmembrane domain"
XX
PN   US5672355-A.
XX
PD   30-SEP-1997.
XX
PF   22-DEC-1993;   93US-00171763.
XX
PR   22-AUG-1989;   89US-00397689.
PR   18-OCT-1991;   91US-00779500.
PR   19-DEC-1991;   91US-00811422.
XX
PA   (VETE-) VETERINARY INFECTIOUS DISEASE.
XX
PI   Babiuk LA.  Parkst MD,  Cox GJ;
XX
DR   WPI; 1997-488823/45.
DR   N-PSDB; AAT89387.
DR   PC:NCBI; gi17529675.
DR   PC:SWISSPROT; P25193.
XX
PT   Vaccines against bovine coronavirus - containing recombinant bovine
PT   coronavirus polypeptide(s).
XX
PS   Claim 13; Fig 9; 52pp; English.
XX
CC   This polypeptide comprises the E2 protein, also designated peplomer
CC   protein or S (Spike), of bovine coronavirus (BCV). It has a mol.wt. of
CC   150 kDa exclusive of glycosylation and contains 21 potential N-linked
CC   glycosylation sites. The amino acid sequence was deduced from an clone E2
CC   cDNA (see AAT89387). The E2 gene in plasmid pT18E2 (E. coli JM105) is
CC   deposited as ATCC 68041. The BCV E3 gene (see AAT89388) is immediately 5'
CC   of the E2 gene on the viral genome and terminates 14 nucleotides upstream
CC   from the E2 initiation codon. The E2 and E3 genes have been cloned and
CC   can be used for the recombinant production of BCV polypeptides, using
CC   e.g. Spodoptera frugiperda Sf9 insect cells as host cells. Glycosylated
CC   and non-glycosylated recombinant E2 and E3 (see AAW31707) are useful as
CC   components of vaccines directed toward preventing BCV infection, or
CC   reducing the severity of BCV infection, in bovine populations. (Updated
CC   on 25-MAR-2003 to correct PF field.)
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CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 1363 AA;

  Query Match             95.2%;  Score 6965;  DB 2;  Length 1363;
  Best Local Similarity   95.4%;  Pred. No. 0;
  Matches 1300;  Conservative   25;  Mismatches   38;  Indels    9;  Gaps    0;

Qy          1 MFLILLISLPMAFAVIGDLKCTTVSINDVDTGAPSISTDVVDVTNGLGTYYVLDRVYLNT 60
              |||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db          1 MFLILLISLPMAFAVIGDLKCTTVSINDVDTGAPSISTDIVDVTNGLGTYYVLDRVYLNT 60

Qy         61 TILLNGYYPTSGSTYRNMALKGTLLLSTLWFKPPFLSDFIDGVFAKVKNTKVIKDGVVYS 120
              |:||||||||||||||||||||||||| ||||||||||||:|:||||||||||| ||:||
Db         61 TLLLNGYYPTSGSTYRNMALKGTLLLSRLWFKPPFLSDFINGIFAKVKNTKVIKKGVMYS 120

Qy        121 EFPAITIGSTFVNISYSVVVQPHTTNLDNKLQGLLEISVCQYTMCDYPHTMCHPNLGNKR 180
              ||||||||||||||||||||||||:||||||||||||||||||||:||||:||| |||||
Db        121 EFPAITIGSTFVNISYSVVVQPHTINLDNKLQGLLEISVCQYTMCEYPHTICHPKLGNKR 180

Qy        181 IELNHWDTGVVPCLYKRNFTYDVNADYLYSHFYQEGGIFYAYFTDTGVVTKFLFHVYLGT 240
              :|||||||||| ||||||||||||||||| ||||||| ||||||||||||||||||||||
Db        181 VELNHWDTGVVSCLYKRNFTYDVNADYLYFHFYQEGGTFYAYFTDTGVVTKFLFNVYLGT 240

Qy        241 VISHYYVMPLTCNSAMTLEYWVTPLTFKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLS 300
              |:|||||:||||:||:|||||||||| |||||||||||||||||||||||||||||||||
Db        241 VLSHYYVLPLTCSSANTLEYWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLS 300

Qy        301 IAPSTGVYELNGYTVQPIADVYRRIPNLPDCNIEANLNDKSVPSPLNWERKTFSNCNFNM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 IAPSTGVYELNGYTVQPIADVYRRIPNLPDCNIEANLNDKSVPSPLNWERKTFSNCNFNM 360

Qy        361 SSLMSFIQADSFTCNNIDAAKIYGMCFFSITIDKFAIPNGRKVDLQMGNLGYLQSFNYRI 420
              ||||||||||||||||||||||||||| ||||||||||||||||||:|||||||||||||
Db        361 SSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFNYRI 420

Qy        421 DTTATSCQLYYNLPASNVSISRFNPSIWNRRFGFTEQSVFKPQPVGVFTDHDVVYAQHCF 480
              |||||||||||||||:|||:|||||| |||||||||| ||||||||||| ||||||||||
Db        421 DTTATSCQLYYNLPAANVSVSRFNPSTWNRRFGFTEQFVFKPQPVGVFTHHDVVYAQHCF 480

Qy        481 KAPTNFCPCKLNGSLCVGSGFGIDAGYKNSGIGTCPAGTNYLTCYNANQCDCLCTPDPIL 540
              ||| |||||||:||||||:| |||||||||||||||||||||||:|| ||||||||||| 
Db        481 KAPKNFCPCKLDGSLCVGNGPGIDAGYKNSGIGTCPAGTNYLTCHNAAQCDCLCTPDPIT 540

Qy        541 SFSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPKAFLGWSVDSCLQGDRCNI 600
              |:|||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        541 SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPQAFLGWSVDSCLQGDRCNI 600

Qy        601 FANFILHGVNSGTTCSTDLQKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNSWQNLL 660
              ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 FANFIFHDVNSGTTCSTDLQKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNSWQNLL 660

Qy        661 YDSNGNLYGFRDYITNRTFMIRSCYSGRVSAGFHSNSSEPALLFRNIKCNYVFNNTLSRQ 720
              ||||||||||||||||||||||||||||||| ||:|||||||||||||||||||||||||
Db        661 YDSNGNLYGFRDYITNRTFMIRSCYSGRVSAAFHANSSEPALLFRNIKCNYVFNNTLSRQ 720

Qy        721 LQPINYFDSYLGCVVNADNSTSSSVQTCDLTVGSGYWGDYSTQRRSRRTITTGYRFTNFE 780
              ||||||||||||||||||||||| ||||||||||||  ||||:||||| |||||||||||
Db        721 LQPINYFDSYLGCVVNADNSTSSVVQTCDLTVGSGYCVDYSTKRRSRRAITTGYRFTNFE 780

Qy        781 PFTVNPVNDSLHPVGGLYEIQIPSEFTIGNMEEFIQTRSPKVTIDCPVFVCGDYAACKSQ 840
              ||||| ||||| ||||||||||||||||||||||||| ||||||||  ||||||||||||
Db        781 PFTVNSVNDSLEPVGGLYEIQIPSEFTIGNMEEFIQTSSPKVTIDCSAFVCGDYAACKSQ 840

Qy        841 LVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGFNFNVDDINFSPVL 900
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db        841 LVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGVNFNVDDINFSPVL 900
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Qy        901 GCLGSECNFVSSRSAIEDLLFSKVKLSDVGFVDAYNMCTGGAEIRDLICVQSYNGIKVLP 960
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCLGSACNKVSSRSAIEDLLFSKVKLSDVGFVEAYNMCTGGAEIRDLICVQSYNGIKVLP 960

Qy        961 PLLSEMQISGYTLAATFASLFPPWSAAAGVPFTLMVQYKINGIGVTMDVLTQMQKLISNA 1020
              |||| |||||||||||| |||||| ||| ||||||||||||||||||||||:|||||:|||
Db        961 PLLSVNQISGYTLAATSASLFPPLSAAVGVPFYLNVQYRINGIGVTMDVLSQMQKLIANA 1020

Qy       1021 FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISASLQEILSRLDA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db       1021 FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRLDA 1080

Qy       1081 LEAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINFCGNG 1140
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1081 LEAQAQIDRLINGRLTALNVYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINFCGNG 1140

Qy       1141 NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT 1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT 1200

Qy       1201 GSGYYYPEPITGNNVVVMSTCAVNYTKADVMLNISTPHLPDFKEELDQWFKNQTSVAPD 1260
              |||||||||||||||||||||||||||||||||||||| |||||||||||| :|||||||
Db       1201 GSGYYYPEPITGNNVVVNSTCAVNYIKADVMLNISTPNLHDFKEELDQWFKNQTSVAPD 1260

Qy       1261 LSLDYINVTFLDLQDEMNRLQEAIKVLNHSYINLKDIGTYEYYVKWPWYVWLLIGLAGVA 1320
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1261 LSLDYINVTFLDLQDEMNRLQEAIKVLNQSYINLKDIGIYEYYVKWPWYVWLLIGFAGVA 1320

Qy       1321 MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD 1363
              ||||||||||||||||| ||||||||||||||||||||||||||
Db       1321 MLVLLFFICCCTGCGTSCFKICGGCCDDYTGHQELVIKTSHDD 1363
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